#5
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/502,424

DATE: 11/28/2000
TIME: 14:51:08

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3 <110> APPLICANT: Kilian, Andrzej
4 Bowtell, David
7 <120> TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES
8 THEREOF
10 <130> FILE REFERENCE: 190106.407
12 <140> CURRENT APPLICATION NUMBER: 09/502,424
13 <141> CURRENT FILING DATE: 2000-02-11
15 <150> PRIOR APPLICATION NUMBER: US 09/108,401
16 <151> PRIOR FILING DATE: 1998-06-30
19 <160> NUMBER OF SEQ ID NOS: 155
21 <170> SOFTWARE: PatentIn Ver. 2.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 3964
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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32 gacgcacggc cgccccccgc cgccccctcc ttccgccagg tgtcctgcct gaaggagctg 240
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97 <210> SEQ ID NO: 2
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99 <212> TYPE: PRT
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107 20 25 30
109 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
110 35 40 45
112 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
113 50 55 60

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118 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
119                  85                  90                  95
121 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
122             100                 105                 110
124 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
125         115                 120                 125
127 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
128     130                 135                 140
130 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
131 145                 150                 155                 160
133 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
134                 165                 170                 175
136 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
137             180                 185                 190
139 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
140         195                 200                 205
142 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
143     210                 215                 220
145 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
146 225                 230                 235                 240
148 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
149                 245                 250                 255
151 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
152             260                 265                 270
154 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
155         275                 280                 285
157 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
158     290                 295                 300
160 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
161 305                 310                 315                 320
163 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
164                 325                 330                 335
166 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
167             340                 345                 350
169 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
170         355                 360                 365
172 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
173     370                 375                 380
175 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
176 385                 390                 395                 400
178 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
179                 405                 410                 415
181 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
182             420                 425                 430
184 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
185         435                 440                 445
187 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
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190 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
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193 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
194                 485                 490                 495
196 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
197             500                 505                 510
199 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
200         515                 520                 525
202 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
203     530                 535                 540
205 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
206 545                 550                 555                 560
208 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
209                 565                 570                 575
211 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
212             580                 585                 590
214 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
215         595                 600                 605
217 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
218     610                 615                 620
220 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
221 625                 630                 635                 640
223 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
224                 645                 650                 655
226 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
227             660                 665                 670
229 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
230         675                 680                 685
232 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
233     690                 695                 700
235 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
236 705                 710                 715                 720
238 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
239                 725                 730                 735
241 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
242             740                 745                 750
244 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
245         755                 760                 765
247 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
248     770                 775                 780
250 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
251 785                 790                 795                 800
253 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
254                 805                 810                 815
256 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
257             820                 825                 830
259 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
260         835                 840                 845
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262 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
263     850                 855                 860
265 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
266 865                 870                 875                 880
268 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
269                 885                 890                 895
271 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
272             900                 905                 910
274 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
275         915                 920                 925
277 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
278     930                 935                 940
280 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
281 945                 950                 955                 960
283 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
284                 965                 970                 975
286 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
287             980                 985                 990
289 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
290         995                 1000                1005
292 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
293    1010                1015                1020
295 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
296 1025                1030                1035                1040
298 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
299                 1045                1050                1055
301 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
302             1060                1065                1070
304 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
305         1075                1080                1085
307 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
308     1090                1095                1100
310 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
311 1105                1110                1115                1120
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314                 1125                1130
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318 <211> LENGTH: 1031
319 <212> TYPE: PRT
320 <213> ORGANISM: Euplotes aediculatus
322 <400> SEQUENCE: 3
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327             20                  25                  30
329 Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
330         35                  40                  45
332 Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
333     50                  55                  60
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VERIFICATION SUMMARY
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L:9332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91
L:9369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:93
L:9411 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95